

#2

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/964,277

DATE: 10/10/2001  
TIME: 13:54:55

Input Set : A:\434.app.txt  
Output Set: N:\CRF3\10102001\I964277.raw

4 <110> APPLICANT: Luche, Ralf M.  
5 Wei, Bo  
7 <120> TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE  
10 <130> FILE REFERENCE: 200125.434  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/964,277  
13 <141> CURRENT FILING DATE: 2001-09-25  
15 <160> NUMBER OF SEQ ID NOS: 22  
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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20 <211> LENGTH: 3496  
21 <212> TYPE: DNA  
22 <213> ORGANISM: Homo sapiens  
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27 gagggggggcc cgaggggaga cggcgtgaca actttcggtt ccctctgagg gaattgggag 180  
28 gtcggcggcc cccaaagctt tcagtccagt gtaaaagctgt tggagcgcgg gagcaaagg 240  
29 aaagaatgat gtaatgcgt gcgtgcgtcca aagcatcttt tggttgaaa tggttattcc 300  
30 agtcatctct ttatgaatca aatgtgaggg gctgcgttgt ggacggagtc ctgtcaaga 360  
31 gcacatcaac gggaaagaga aagagacatt cacttggagg gctcttgctg aaaatgggtt 420  
32 taactctcct ttgccagtc accaccagcc tgacctata cacttttagt acaatggagt 480  
33 ggctgagcct ttgagcacac caccattaca tcacgtggc aaattaaaga aggaggtggg 540  
34 aaaagaggac ttattgttgt catggcccat gagatgattt gaaactcaaat tgttactgag 600  
35 aggttgggtt ctctgttggaa aagtggaaacg gaaaaagtgc tgctaatttga tagccggcca 660  
36 tttgttggaaat acaatacatac ccacatttttgaagccatta atatcaactg ctccaaagctt 720  
37 atgaagcgaa ggttgcacaac ggacaaagtgt ttaattacag agctcatcca gcattcagcg 780  
38 aaacataagg ttgacatttga ttgcagtcaag aaggttggtag tttacatca aagctccaa 840  
39 gatgttgcct ctctcttcc agactgtttt ctcactgtac ttctgggtaa actggagaag 900  
40 agcttcaact ctgttccacct gcttgcaggt gggtttgcgt agttctctcg ttgtttccct 960  
41 ggcctctgtg aaggaaaatc cactctagtc cctacccgtca ttctcgacc ttgttttacct 1020  
42 gttgccaaca ttggccaac ccgaatttctt cccaaatcttt atcttggctg ccagcgagat 1080  
43 gtccctcaaca aggagctgtat gcacgcgaaat gggattgggtt atgtgttaaa tgccagcaat 1140  
44 acctgtccaa agcctgactt tatccccgag ttcatttcc tgcgtgtgcc tgtgaatgac 1200  
45 agcttttgtt agaaaatttt gccgtggttt gacaaatcag tagatttcat tgagaaagca 1260  
46 aaagcctcca atggatgtgt tctagtgac ttttagctg ggatctccc ctccggccacc 1320  
47 atcgctatcg cctacatcat gaagaggatg gacatgtctt tagatgaagc ttacagattt 1380  
48 gtggaaagaaa aaagacctac tatatctcca aacttcaatt ttctggccca actcctggac 1440  
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50 ctgcacccgtt agaagccaaa tgaacctgtc cctgtgtctt cagagggtgg acagaaaagc 1560  
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52 cccgtgcata cccgcgcgtt gcccagcgtt cccagcgtgc agccgtcgct tttagaggac 1680  
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54 aataagctca agegttccctt ctctctggat atcaaatcag tttcatatttgc agccacatg 1800  
55 gcagcatcct tacatggctt ctccatca gaagatgctt tggaaatacta caaaccttcc 1860  
56 actactctgg atggaccaa caagctatgc cagttctccc ctgttcaggaa actatcgag 1920  
57 cagactcccg aaaccagtcc tgataaggag gaagccagca tccccaagaaa gctgcagacc 1980  
58 gccaggcctt cagacagccaa gagcaagcga ttgcattcgg tcagaaccag cagcagtggc 2040

ENTERED

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Input Set : A:\434.app.txt  
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59 accgcccaga ggtccctttt atctccactg catcgaagtggagacaaattac 2100  
 60 cacaccagct tcctttcgg cctttccacc agccagcagc acctcacgaa gtctgctggc 2160  
 61 ctgggcctta aggctggca ctcggatatac ttggcccccc agacctctac cccttccctg 2220  
 62 accagcagct ggtattttgc cacagagtcc tcacacttct actctgcctc agccatctac 2280  
 63 ggaggcagtg ccagttactc tgcctacagc tgccagcagc tgcccaacttgcggagacaa 2340  
 64 gtctattctg tgcgcaggcg gcagaagcca agtgacagag ctgactcgcg gcggagctgg 2400  
 65 catgaagaga gccccttga aaagcagttt aaacgcagaa gctgccaaat ggaattttgga 2460  
 66 gagagcatca tgtcagagaa caggtcacgg gaagagctgg ggaaagtggg cagtcagtct 2520  
 67 agctttcgg gcagcatgga aatcatttagg gtctcctgag aagaaaagaca ctttgtactt 2580  
 68 ctataagacaa ttttttttc ttgttcacaa aaaaattccc tgtaaatctg aaatatataat 2640  
 69 atgtacatac atatatattt ttggaaaaatg gagctatggt gtaaaagcaa caggtggatc 2700  
 70 aacccagttt ttactctt aacatctgca tttgagagat cagctaatac ttctctcaac 2760  
 71 aaaaatggaa gggcagatgc tagaatcccc cctagacgga ggaaaaccat tttattcagt 2820  
 72 gaattacaca tcctctgtt cttaaaaaaag caagtgtctt ttgtgttggg ggacaaaatc 2880  
 73 ccctaccatt ttccacgtt tgctactaag agatctaaa tattagtctt tgcggacc 2940  
 74 cttccatagt acaccttagc gctgagactg agccagcttggggtcagg aggtagaccc 3000  
 75 tggtagggac agagcctagt ggtttatcca agagaaatgatccttatccaa agctgattca 3060  
 76 caaacccacg ctcacatgac agccgaggga cacgagcatac actctgtgg acggaccatt 3120  
 77 agggccttgc caaggtcta ctttagagca aacccagtagc ctcagacagg aaagtcgggg 3180  
 78 cttgaccac taccatatct ggtagccat tttcttaggca ttgtgaatag gtaggttagct 3240  
 79 agtcacactt ttcagaccaa ttcaaaactgt ctatgcacaa aattccctgtt ggccttagatg 3300  
 80 gagataattt tttttcttc tcagctttat gaagagaagg gaaactgtct aggattcagc 3360  
 81 tgaaccacca ggaacctggc aacatcacga tttaagctaa ggttgggagg ctaacgagtc 3420  
 82 tacctccctc ttgttaatc aaagaattgt ttaaaatggg attgtcaatc cttaaataaa 3480  
 83 agatgaactt ggttc 3496  
 85 <210> SEQ ID NO: 2  
 86 <211> LENGTH: 665  
 87 <212> TYPE: PRT  
 88 <213> ORGANISM: Homo sapiens  
 90 <400> SEQUENCE: 2  
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 92 1 5 10 15  
 93 Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg  
 94 20 25 30  
 95 Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile  
 96 35 40 45  
 97 Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu  
 98 50 55 60  
 99 Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp  
 100 65 70 75 80  
 101 Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala  
 102 85 90 95  
 103 Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu  
 104 100 105 110  
 105 Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe  
 106 115 120 125  
 107 Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro  
 108 130 135 140  
 109 Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr

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110	145	150	155	160
111	Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn			
112	165	170	175	
113	Lys Glu Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser			
114	180	185	190	
115	Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg			
116	195	200	205	
117	Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp			
118	210	215	220	
119	Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val			
120	225	230	235	240
121	Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile			
122	245	250	255	
123	Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg			
124	260	265	270	
125	Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Leu			
126	275	280	285	
127	Gly Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala			
128	290	295	300	
129	Ser Gly Pro Lys Ser Lys Leu Lys Leu His Leu Glu Lys Pro Asn			
130	305	310	315	320
131	Glu Pro Val Pro Ala Val Ser Glu Gly Gln Lys Ser Glu Thr Pro			
132	325	330	335	
133	Leu Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln			
134	340	345	350	
135	Arg Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro			
136	355	360	365	
137	Ser Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His			
138	370	375	380	
139	Leu Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe			
140	385	390	395	400
141	Ser Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser			
142	405	410	415	
143	Leu His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro			
144	420	425	430	
145	Ser Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val			
146	435	440	445	
147	Gln Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu			
148	450	455	460	
149	Ala Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln			
150	465	470	475	480
151	Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly Thr Ala Gln			
152	485	490	495	
153	Arg Ser Leu Leu Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn			
154	500	505	510	
155	Tyr His Thr Ser Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu			
156	515	520	525	
157	Thr Lys Ser Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu			
158	530	535	540	

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159 Ala Pro Gln Thr Ser Thr Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala  
 160 545 550 555 560  
 161 Thr Glu Ser Ser His Phe Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Ser  
 162 565 570 575  
 163 Ala Ser Tyr Ser Ala Tyr Ser Cys Ser Gln Leu Pro Thr Cys Gly Asp  
 164 580 585 590  
 165 Gln Val Tyr Ser Val Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp  
 166 595 600 605  
 167 Ser Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys  
 168 610 615 620  
 169 Arg Arg Ser Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn  
 170 625 630 635 640  
 171 Arg Ser Arg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser  
 172 645 650 655  
 173 Gly Ser Met Glu Ile Ile Glu Val Ser  
 174 660 665  
 177 <210> SEQ ID NO: 3  
 178 <211> LENGTH: 156  
 179 <212> TYPE: PRT  
 180 <213> ORGANISM: Homo sapiens  
 182 <400> SEQUENCE: 3  
 183 Asp Gly Ser Pro Leu Ser Asn Ser Gln Pro Ser Phe Pro Val Glu Ile  
 184 1 5 10 15  
 185 Leu Pro Phe Leu Tyr Leu Gly Cys Ala Lys Asp Ser Thr Asn Leu Asp  
 186 20 25 30  
 187 Val Leu Glu Glu Phe Gly Ile Lys Tyr Ile Leu Asn Val Thr Pro Asn  
 188 35 40 45  
 189 Leu Pro Asn Leu Phe Glu Asn Ala Gly Glu Phe Lys Tyr Lys Gln Ile  
 190 50 55 60  
 191 Pro Ile Ser Asp His Trp Ser Gln Asn Leu Ser Gln Phe Phe Pro Glu  
 192 65 70 75 80  
 193 Ala Ile Ser Phe Ile Asp Glu Ala Arg Gly Lys Asn Cys Gly Val Leu  
 194 85 90 95  
 195 Val His Cys Leu Ala Gly Ile Ser Arg Ser Val Thr Val Thr Val Ala  
 196 100 105 110  
 197 Tyr Leu Met Gln Lys Leu Asn Leu Ser Met Asn Asp Ala Tyr Asp Ile  
 198 115 120 125  
 199 Val Lys Met Lys Lys Ser Asn Ile Ser Pro Asn Phe Asn Phe Met Gly  
 200 130 135 140  
 201 Gln Leu Leu Asp Phe Glu Arg Thr Leu Gly Leu Ser  
 202 145 150 155  
 205 <210> SEQ ID NO: 4  
 206 <211> LENGTH: 156  
 207 <212> TYPE: PRT  
 208 <213> ORGANISM: Homo sapiens  
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 211 Asp Gly Ser Pro Val Pro Ser Ser Gln Pro Ala Phe Pro Val Gln Ile  
 212 1 5 10 15  
 213 Leu Pro Tyr Leu Tyr Leu Gly Cys Ala Lys Asp Ser Thr Asn Leu Asp

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214          20          25          30
215 Val Leu Gly Lys Tyr Gly Ile Lys Tyr Ile Leu Asn Val Thr Pro Asn
216          35          40          45
217 Leu Pro Asn Ala Phe Glu His Gly Gly Glu Phe Thr Tyr Lys Gln Ile
218          50          55          60
219 Pro Ile Ser Asp His Trp Ser Gln Asn Leu Ser Gln Phe Phe Pro Glu
220 65          70          75          80
221 Ala Ile Ser Phe Ile Asp Glu Ala Arg Ser Lys Lys Cys Gly Val Leu
222          85          90          95
223 Val His Cys Leu Ala Gly Ile Ser Arg Ser Val Thr Val Thr Val Ala
224          100         105         110
225 Tyr Leu Met Gln Lys Met Asn Leu Ser Leu Asn Asp Ala Tyr Asp Phe
226          115         120         125
227 Val Lys Arg Lys Lys Ser Asn Ile Ser Pro Asn Phe Asn Phe Met Gly
228          130         135         140
229 Gln Leu Leu Asp Phe Glu Arg Thr Leu Gly Leu Ser
230 145          150          155
233 <210> SEQ ID NO: 5
234 <211> LENGTH: 156
235 <212> TYPE: PRT
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 5
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241 Leu Pro Asn Leu Tyr Leu Gly Ser Ala Arg Asp Ser Ala Asn Leu Glu
242          20          25          30
243 Ser Leu Ala Lys Leu Gly Ile Arg Tyr Ile Leu Asn Val Thr Pro Asn
244          35          40          45
245 Leu Pro Asn Phe Phe Glu Lys Asn Gly Asp Phe His Tyr Lys Gln Ile
246          50          55          60
247 Pro Ile Ser Asp His Trp Ser Gln Asn Leu Ser Arg Phe Phe Pro Glu
248 65          70          75          80
249 Ala Ile Glu Phe Ile Asp Glu Ala Leu Ser Gln Asn Cys Gly Val Leu
250          85          90          95
251 Val His Cys Leu Ala Gly Val Ser Arg Ser Val Thr Val Thr Val Ala
252          100         105         110
253 Tyr Leu Met Gln Lys Leu His Leu Ser Leu Asn Asp Ala Tyr Asp Leu
254          115         120         125
255 Val Lys Arg Lys Lys Ser Asn Ile Ser Pro Asn Phe Asn Phe Met Gly
256          130         135         140
257 Gln Leu Leu Asp Phe Glu Arg Ser Leu Arg Leu Glu
258 145          150          155
261 <210> SEQ ID NO: 6
262 <211> LENGTH: 155
263 <212> TYPE: PRT
264 <213> ORGANISM: Homo sapiens
266 <400> SEQUENCE: 6
267 Leu Ser Gln Pro Cys Leu Pro Val Pro Ser Val Gly Leu Thr Arg Ile
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**VERIFICATION SUMMARY**

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Input Set : A:\434.app.txt

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L:12 M:270 C: Current Application Number differs, Wrong Format